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ClustalW Results

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SEQIDNO:6
gi13448825|JAM3

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO_6 310 aa

Sequence 2: gi13448825|JAM3 310 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:4221

Alignment Score 1954

CLUSTAL-Alignment file created [baaiPaWsX.aln]

CLUSTAL W (1.7) multiple sequence alignment

```
SEQIDNO_6      MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
gi13448825|JAM3 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
*****
```

```
SEQIDNO_6      SDPRI EWKKIQDEQTTYVFFDNKI QGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVAR
gi13448825|JAM3 SDPRI EWKKIQDEQTTYVFFDNKI QGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVAR
*****
```

```
SEQIDNO_6      NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL
gi13448825|JAM3 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL
*****
```

```
SEQIDNO_6      PTDSRANPRFRNSSSHLNSSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL
gi13448825|JAM3 PTDSRANPRFRNSSSHLNSSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL
*****
```

SEQIDNO_6
gi13448825|JAM3
NIGGIIGGVLVVLAVLALITLGICCA YRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG
NIGGIIGGVLVVLAVLALITLGICCA YRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG

SEQIDNO_6
gi13448825|JAM3
DFRHKSSFVI
DFRHKSSFVI

Submit sequences to:





ClustalW Results

Sequences Help

Retrieval BLAST2 FASTA ClustalW DCS Assembly Phlip Translation

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SEQINDO:25
g113448824|JAM3

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: SEQINDO_25 1956 bp
Sequence 2: g113448824|JAM3 933 bp
Start of Pairwise Alignments
Aligning...
Sequences (1:2) Aligned. Score: 99
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2 Score:17708
Alignment Score 6691
CLUSTAL-Alignment file created [bsat2a4ex.aln]
CLUSTAL W (1.7) multiple sequence alignment

SEQINDO_25 CCGGACATCAAGCCGCGCGCGCTGCGCCCTGACGACACCTTGACATGAGCGCT
g113448824|JAM3 -----ATGGCGCT

SEQINDO_25 GAGCGGCGCACCGCGCATCCCGCTGCGCGCTGCGCGCTGCGCATCTTCTGCTGCTGCT
g113448824|JAM3 GAGCGGCGCACCGCGCATCCCGCTGCGCGCTGCGCGCTGCGCATCTTCTGCTGCTGCT

SEQINDO_25 TTTCAAGGCGCTGCGCTGATGAGGCGCTGTAATCTCAAAATCCAGCAATCGAACCCGATGAT
g113448824|JAM3 TTTCAAGGCGCTGCGCTGATGAGGCGCTGTAATCTCAAAATCCAGCAATCGAACCCGATGAT

SEQINDO_25 ACAGCAATTTGAAAGTGTGAACTGTCTTGCATCATTCAGATTCGAGACAGATGATGCC
g113448824|JAM3 ACAGCAATTTGAAAGTGTGAACTGTCTTGCATCATTCAGATTCGAGACAGATGATGCC

SEQINDO_25 CAGATCGATGAGAGAAAATTCAAGATGACAAACCACTATGTGTTTTTGAACACAA
g113448824|JAM3 CAGATCGATGAGAGAAAATTCAAGATGACAAACCACTATGTGTTTTTGAACACAA

SEQINDO_25 AATTCAAGGAGACTTGGCGGGTGTGTCAAGAAATACCTGGGAAAGCATCCCTGAAATGTG
g113448824|JAM3 AATTCAAGGAGACTTGGCGGGTGTGTCAAGAAATACCTGGGAAAGCATCCCTGAAATGTG

SEQINDO_25 GAATGTGACACGAGAGACTACGCGCTTATTCCTGTGAGGTGCTGTGCTGCAAAATGACCG
g113448824|JAM3 GAATGTGACACGAGAGACTACGCGCTTATTCCTGTGAGGTGCTGTGCTGCAAAATGACCG

SEQINDO_25 CAAGCAAAATTGATGATTTGTGATTCGATGATTAACGTGTCAATGTAAGCCGATGACCCCTGT
g113448824|JAM3 CAAGCAAAATTGATGATTTGTGATTCGATGATTAACGTGTCAATGTAAGCCGATGACCCCTGT

SEQINDO_25 CTGTGAGGTGCTGGAAGGCTGTGACATGTAAGCAAGATGGCAACATGCACTGTGCAAGAGAG
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SEQINDO_25 TGAAGGCGCACCCCGGCTCACTACACAGCTGTGATCGAATGATACATGACCTGCCAGGA
g113448824|JAM3 TGAAGGCGCACCCCGGCTCACTACACAGCTGTGATCGAATGATACATGACCTGCCAGGA

SEQINDO_25 TTCCAGAGCCAAATCCAGATTCGCAATTCCTTCCCACTTAACTGTGAACAGGCAC
g113448824|JAM3 TTCCAGAGCCAAATCCAGATTCGCAATTCCTTCCCACTTAACTGTGAACAGGCAC

SEQINDO_25 TTTGTGTGCTACTGTGTTCACAAAGGACATCTGTGGGAGATGATACGATGATGCTTCCAA
g113448824|JAM3 TTTGTGTGCTACTGTGTTCACAAAGGACATCTGTGGGAGATGATACGATGATGCTTCCAA

SEQINDO_25 TGAACCAAGCTCAACAGGTGTGAGGACAGAGAGATGAAAGTCTATGACATGACATTTGG
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SEQINDO_25 CGGAATTAATTTGGGGGGGTTCTGTGTGTCTTGTGCTGTGATCGGCTGATTCAGGTGGGAT
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SEQINDO_25 CTGCTGTGCTATGACAGAGTGTGCTATCAACAAATTAACAGAGATGAGAAATTTTCAAA
g113448824|JAM3 CTGCTGTGCTATGACAGAGTGTGCTATCAACAAATTAACAGAGATGAGAAATTTTCAAA

SEQINDO_25 GAAACCAAGGAAACAGATGAGATTTATCAATCCGACATGACAGAGAGGCGATTCAG
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SEQINDO_25 GTGCACAAATCTGTGAGAAATCTGCTGTCAATGAGGACAGAGATGACATCTGAGAGAG
g113448824|JAM3 GTGCACAAATCTGTGAGAAATCTGCTGTCAATGAGGACAGAGATGACATCTGAGAGAG

SEQINDO_25 AGCTAGACATCATTCAGAAACCTTTTCGTTTGGCCAAAGTTGACACATCTCTTTTAC
g113448824|JAM3 AGCTAGACATCATTCAGAAACCTTTTCGTTTGGCCAAAGTTGACACATCTCTTTTAC

Submit sequences to: BLAST2



Submit

Reset



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SBQIDNO.25
g113448824|JMK3
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SBQIDNO.25
g113448824|JMK3
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AAGAAACGAAACTGGGTGCTTCACTGATGGGTCTTAATCTGTTCGTGGCTGATTT
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SBQIDNO.25
g113448824|JMK3
-----
CCCGCATGATATTTAGGTGATCTTAAAGATTTGCTCACTTAACCCCGTGTGGGC
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SBQIDNO.25
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SBQIDNO.25
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SBQIDNO.25
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SBQIDNO.25
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SBQIDNO.25
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SBQIDNO.25
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SBQIDNO.25
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SBQIDNO.25
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